

SEQUENCE LISTING

<110> Rupert, PFALLER

<120> pyrF GENE AND ITS USE

<130> PFALLER-1 US PCT

<150> PCT/EP00/06091

<151> 2000-06-29

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 3448

<212> DNA

<213> Trametes versicolor

<220>

<221> gene

<222> (1133)..(1877)

<223>

<220>

<221> promoter

<222> (1)..(1132)

<223>

<220>

<221> 3'UTR

<222> (1878)..(3448)

<223>

<220>

<221> Intron

<222> (1226)..(1286)

<223>

<400> 1

gatctcgagt aggatggaga acggtataac gatgccagag atgataggtg tccagcggta 60

gttgggaacg aggctgtcta ggtcggcggt cttgtcgtcg gtcggccaga ggtacgattt 120

gagggcagag tatagagata tccctaggag tgtgacgtca tcggacgagt taccctccgc 180

ggtatgttgt gtactgtcca ccttctccgg gtcagacggg tgtgatgtac tgcgtccggg 240

ttggagcgtc aggaaaagcg cagacaggct gaagagtccc attccgccgc agaaggtgtg 300

cgagggggaa agtgccagtg tagcagtgag gcgtgcctac gatatgagac ggacatggtc 360

agtatctatg cccggtcaag gtcgccgcac agacctcact gtaacctcat ggcaatgtcg 420
 cggatgcaca aagcaggtag agatgttcaa atggggcacg gagcgggtcg tccggagcgc 480
 tctccctcgg ctctttgcaa ggcagctggc ggatgtttgg tcagttgagg tactgcatcc 540
 cttgcaatag cgaaaacagc tcaccagacg tgagtatatg ctgtatacgg gagaaggaag 600
 cggaacaccg tgagtggaag agatgaagtg gttatgaata catcccgggtg gaggttgagt 660
 ctaacagcgt cggatctcgc tgcgttccgg agcagaggcc cggtagcagc gccggtgtct 720
 gtcgtgttcc cggcacgccg tatgctcgta aatcaccttt agaaaacttg aataagtgaag 780
 agaagatacg aaacgtcagt ctgcacctat ggagatatgt aaaaatcgca aaaacatagc 840
 gttgacgcta taaaaaagaa aaggacaaaa tgaccaccgc aggggtcgaa cctgcaatct 900
 cctgatccct aggtttgaag gttcatcacc tcaattcgta gtcagacgcg atgccatttc 960
 gccaggcggc cgttagaaac gaaactacta cgtttaaacc cgggtataac acagcctagt 1020
 attccgtgcg ggccgcgccg ccgataagct tgttttcgtg aactgtcttc cccctcctgc 1080
 atctcgattc tcgacctcca tcgccgcgac gatcccttcc tccccactca ccatgtcgct 1140
 cgaaaaatac cagacagagc tcatcgagca cggcatgacc gccggtgcgc tcaagttcgg 1200
 gaccttcacc ctcaaatacag gccgggtccgt cccctcccta ggctgcgcgc cgctctcccc 1260
 gtgaacgctc cctcaccocg cgcaggacct cgccctactt cttcaacgcc ggctgctcg 1320
 cgtccggggc cgtgctcgac acgctgtgct ccgcgtacgc cgcgacgac gcgcgcgcgc 1380
 tcaaggcgct gcccgggctg cccgcgttcg acgtgctctt cgggcccgcg tacaagggca 1440
 tcccgttcgc ggccggggacc gcgctgctgc tgcaccgcga ccacggcatc accgtcgggt 1500
 tcgcgtacga ccgcaaggag gcgaaggatc atggggaggg cgggatactt gtgggcgcgc 1560
 cggtgagggg caagcgcgtg ctggtgctgg acgacgtcgc gacggcgggc acggcgatcc 1620
 gccaggcgat tgagactgtg acgaaggagg ggggcgaggt cgttggcgcg gtgttgatgc 1680
 tcgatcggca ggaggtgggc aaggagggga agagcacgct tcgggaggtg gaggcgctgt 1740
 tgggcgggaa gggacgtgtg ccgacgatcc tgaggatgaa ggacctcatg aagtgggtgc 1800
 aggagcacgg ccggacggag gagcttgcca agatgcaaga gtactgggag cagtacggcg 1860
 cgaaggaaag cgaatgagaa gacacgaagg cagttgtgta ctaggtgagt aacaccacgc 1920

tacatcgatc catccactaa acccatgcag atgaagaccc actgtacaat ttctcggtag	1980
ctgtcacggt gaacgcaaag agccgaagat gtgagagtac acatgccatt catccccgata	2040
tatagcacia gaacatgtag taatagaacc tgcagaaaca caaagcatga tcagcaagac	2100
tccatgggca ctgagttatg atgaactaac cgctatcacc aaaaacaccg ctcttattcg	2160
cccaaccgac gaccggaacc ccagttatat cctcccacac cgctcgcagc agcagcagca	2220
gcagcctgct ccctgaccct ccgtgggggc acaacatgca cgcaccacc gacattcgca	2280
acgccccga cccaccctgt cgcgccccca ctagcagact ccccgaaaca cccgcgcagc	2340
cacgcccggc ccgtacctgc agccctgagc gagccggtgt caaagacagt ccaccaccag	2400
aggtggccga cgacagcccc agagatgctg atggcagcgg cgccggggcc gcccatgagg	2460
aggtccatgc cgacgagcat gtagggaagg tagatgacgg ggaaggatg gagcccgaag	2520
aaggatgtct gggaccagc tggggcgagc cgggaggaga cgtaggtgag cgcgaggagg	2580
agcgcgcggg tgtgcacaaa ggtgccgagg ggaatgttga ggccctggtg tgaggcgggt	2640
tagcgcaaaag gtcagaggcg ggatgatact attggacgta cgaggatagc aagtccctgcg	2700
agcgagagct gccatgcgta gtctgaagag cggcggggga agtgtgtctc ttctagctca	2760
ttggaatttc gactagtttc aagtgtacgg tctcagtat catcatgtat tgcaacagtg	2820
tcatacgcac tagagcatcg caaggctcga gatgaagttg atccccgagc ctataaagac	2880
aaggtcagca ccgacatggc atgtagtcag acaagattga gtacgcactt cccaagaaga	2940
agctcgtaaa cactctccag atctacatta agacgtgagt atcgcatacc ttctcagtgc	3000
ctgacttata tttcatccaa ctacagagac agaaaccac ctcaaacttc tgcgtaacga	3060
actccttcac aaagacgacc ttgtatattg gcaagatttg caggagcact ggcaaggatga	3120
cggcgagaga ggaggcgcat agaaaccgag tgactggagg gattttgcga atctcatcca	3180
tgaaagacat cttgaggaga ctggaggatga gtagagcgat agaagtacag caggcagagc	3240
agagacgacg gcagaatgtg ggggaagaaca agcaggagga ggagtagagt gattttgaag	3300
taatgaaaag tggcgcaacc taatgcaaag tgtatgagg acatccgtgg acataaagta	3360
ttccgcacct cgggcaagac attcaatctc agtaatgcac ttcactttcg gagttcaact	3420
tcaaactcga ctttgaaact tgagatcc	3448

<210> 2
 <211> 684
 <212> DNA
 <213> *Trametes versicolor*

<220>
 <221> CDS
 <222> (1)..(684)
 <223>

<400> 2

atg tcg ctc gaa aaa tac cag aca gag ctc atc gag cac ggc atg acc	48
Met Ser Leu Glu Lys Tyr Gln Thr Glu Leu Ile Glu His Gly Met Thr	
1 5 10 15	
gcc ggt gcg ctc aag ttc ggg acc ttc acc ctc aaa tca ggc cgg acc	96
Ala Gly Ala Leu Lys Phe Gly Thr Phe Thr Leu Lys Ser Gly Arg Thr	
20 25 30	
tcg ccc tac ttc ttc aac gcc ggc ctg ctc gcg tcc ggg ccc gtg ctc	144
Ser Pro Tyr Phe Phe Asn Ala Gly Leu Leu Ala Ser Gly Pro Val Leu	
35 40 45	
gac acg ctg tgc tcc gcg tac gcc gcg acg atc gcg cgc gcg ctc aag	192
Asp Thr Leu Cys Ser Ala Tyr Ala Ala Thr Ile Ala Arg Ala Leu Lys	
50 55 60	
gcg tcg ccc ggg ctg ccc gcg ttc gac gtg ctc ttc ggg ccc gcg tac	240
Ala Ser Pro Gly Leu Pro Ala Phe Asp Val Leu Phe Gly Pro Ala Tyr	
65 70 75 80	
aag ggc atc ccg ttc gcg gcg ggg acc gcg ctg ctg ctg cac cgc gac	288
Lys Gly Ile Pro Phe Ala Ala Gly Thr Ala Leu Leu Leu His Arg Asp	
85 90 95	
cac ggc atc acc gtc ggg ttc gcg tac gac cgc aag gag gcg aag gat	336
His Gly Ile Thr Val Gly Phe Ala Tyr Asp Arg Lys Glu Ala Lys Asp	
100 105 110	
cat ggg gag ggc ggg ata ctt gtg ggc gcg ccg gtg agg ggc aag cgc	384
His Gly Glu Gly Gly Ile Leu Val Gly Ala Pro Val Arg Gly Lys Arg	
115 120 125	
gtg ctg gtg ctg gac gac gtc gcg acg gcg ggc acg gcg atc cgc cag	432
Val Leu Val Leu Asp Asp Val Ala Thr Ala Gly Thr Ala Ile Arg Gln	
130 135 140	
gcg att gag act gtg acg aag gag ggg ggc gag gtc gtt ggc gcg gtg	480
Ala Ile Glu Thr Val Thr Lys Glu Gly Gly Glu Val Val Gly Ala Val	
145 150 155 160	

ttg atg ctc gat cgg cag gag gtg ggc aag gag ggg aag agc acg ctt 528
 Leu Met Leu Asp Arg Gln Glu Val Gly Lys Glu Gly Lys Ser Thr Leu
 165 170 175

gcg gag gtg gag gcg ctg ttg ggc ggg aag gga cgt gtg ccg acg atc 576
 Ala Glu Val Glu Ala Leu Leu Gly Gly Lys Gly Arg Val Pro Thr Ile
 180 185 190

ctg agg atg aag gac ctc atg aag tgg ttg cag gag cac ggc cgg acg 624
 Leu Arg Met Lys Asp Leu Met Lys Trp Leu Gln Glu His Gly Arg Thr
 195 200 205

gag gag ctt gcg aag atg caa gag tac tgg gag cag tac ggc gcg aag 672
 Glu Glu Leu Ala Lys Met Gln Glu Tyr Trp Glu Gln Tyr Gly Ala Lys
 210 215 220

gaa agc gaa tga 684
 Glu Ser Glu
 225

<210> 3
 <211> 227
 <212> PRT
 <213> Trametes versicolor

<400> 3

Met Ser Leu Glu Lys Tyr Gln Thr Glu Leu Ile Glu His Gly Met Thr
 1 5 10 15

Ala Gly Ala Leu Lys Phe Gly Thr Phe Thr Leu Lys Ser Gly Arg Thr
 20 25 30

Ser Pro Tyr Phe Phe Asn Ala Gly Leu Leu Ala Ser Gly Pro Val Leu
 35 40 45

Asp Thr Leu Cys Ser Ala Tyr Ala Ala Thr Ile Ala Arg Ala Leu Lys
 50 55 60

Ala Ser Pro Gly Leu Pro Ala Phe Asp Val Leu Phe Gly Pro Ala Tyr
 65 70 75 80

Lys Gly Ile Pro Phe Ala Ala Gly Thr Ala Leu Leu Leu His Arg Asp
 85 90 95

His Gly Ile Thr Val Gly Phe Ala Tyr Asp Arg Lys Glu Ala Lys Asp
100 105 110

His Gly Glu Gly Gly Ile Leu Val Gly Ala Pro Val Arg Gly Lys Arg
115 120 125

Val Leu Val Leu Asp Asp Val Ala Thr Ala Gly Thr Ala Ile Arg Gln
130 135 140

Ala Ile Glu Thr Val Thr Lys Glu Gly Gly Glu Val Val Gly Ala Val
145 150 155 160

Leu Met Leu Asp Arg Gln Glu Val Gly Lys Glu Gly Lys Ser Thr Leu
165 170 175

Ala Glu Val Glu Ala Leu Leu Gly Gly Lys Gly Arg Val Pro Thr Ile
180 185 190

Leu Arg Met Lys Asp Leu Met Lys Trp Leu Gln Glu His Gly Arg Thr
195 200 205

Glu Glu Leu Ala Lys Met Gln Glu Tyr Trp Glu Gln Tyr Gly Ala Lys
210 215 220

Glu Ser Glu
225

<210> 4
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PrimerA

<220>
<221> primer_bind
<222> (1)..(26)
<223> n = i

<220>
<221> misc_feature

<222> (6)..(6)

<223> n = i

<220>

<221> misc_feature

<222> (9)..(9)

<223> n = i

<220>

<221> misc_feature

<222> (12)..(12)

<223> n = i

<220>

<221> misc_feature

<222> (21)..(21)

<223> n = i

<400> 4

ttyggncng cntayaargg nathcc

26

<210> 5

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PrimerB

<220>

<221> primer_bind

<222> (1)..(23)

<223> n = i

<220>

<221> misc_feature

<222> (3)..(3)

<223> n = i

<220>

<221> misc_feature

<222> (6)..(6)

<223> n = i

<220>

<221> misc_feature

<222> (12)..(12)

<223> n = i

<400> 5

ttncncctt cncrtgrtc ytt

23

<210> 6
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PyF-1

<220>
<221> misc_feature
<222> (1)..(35)
<223>

<400> 6
ctagacatgt cgctcgaaaa ataccagaca gagct

35

<210> 7
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PyF-2

<220>
<221> misc_feature
<222> (1)..(35)
<223>

<400> 7
ctgtctggta tttttcgagc gacatgtcta gagct

35